Supplementary Table 1. Subject characteristics of cases and controls undergoing genetic association analyses from the California Childhood Leukemia Study, The Children's Oncology Group, The Wellcome Trust Consortium, the GENEVA Melanoma Study, The University of California, San Francisco Adult Glioma Study, The Mayo Clinic glioma study, and the CGEMS PanScan pancreatic cancer case-control study.

Population	Phase of Study	N (cases/controls)	Ethnicity	Tumor subtype of cases	Genotyping technique	% Male (cases/controls)
California Childhood Leukemia Study	ALL discovery	321/454	Hispanic	B-cell ALL (92.5%) ¹	Illumina OmniExpress	54% / 53%
Children's Oncology Group	ALL validation set 1	980/0	European- ancestry	Unknown	Affymetrix 6.0	51% / -
Wellcome Trust Consortium	ALL validation set 1	0/2624	European- ancestry	-	Affymetrix 6.0	- / 52%
California Childhood Leukemia Study	ALL validation set 2	163/201	African- American (73%) ²	B-cell ALL (86.5%) ³	TaqMan	62% / 62%
M.D. Anderson GENEVA melanoma study	Melanoma case-control analysis	1969/1044	European- ancestry	Invasive melanoma (92.4%) ⁴	Illumina Omni1- Quad	58% / 59%
The UCSF Adult Glioma Study	Glioblastoma case- control analysis	380/547	European- ancestry	Glioblastoma	Pooled next-gen sequencing	65% / 53%
Mayo Clinic glioma case- control study	Glioblastoma case- control analysis	304/274	European- ancestry	Glioblastoma	Pooled next-gen sequencing	62% / 66%
CGEMS PanScan pancreatic cancer case-control samples	Pancreatic cancer case- control analysis	2273/2418	European- ancestry	Pancreatic adenocarcinoma (>85%)	Illumina Human550v3 or 610QuadV1B	52% / 52%

 $^{^{1}}$ 7.5% of ALL patients in the CCLS discovery set had T-cell ALL.

²27% individuals in the CCLS validation sample were Hispanic. Cases and controls were matched on race/ethnicity.

³13.5% of ALL patients in the CCLS validation sample had T-cell ALL.

⁴7.1% of patients were diagnosed with melanoma *in-situ* and 0.51% with atypical melanocytic proliferation.